

# SEQUENCE LISTING

<110> CROCE, Carlo M.  
ISHII, Hideshi

<120> COMPOSITIONS, KITS, AND METHODS RELATING TO THE HUMAN  
FEZ1 GENE, A NOVEL TUMOR SUPPRESSOR GENE

<130> 9855-30U1 (209855.0081)

<140> NOT YET ASSIGNED

<141> 2000-02-25

<150> US 60/121,537

<151> 1999-02-25

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<170> PatentIn Ver. 2.1

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&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln

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70

75

&lt;210&gt; 6

&lt;211&gt; 69

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

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Leu Lys Gln Ala Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His

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<210> 13

<211> 1692

<212> DNA

<213> Homo sapiens

<400> 13

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tccccggaga gtgccagcca ccagctgcac cccgcccctc cagacaagcc caaggagcag 480  
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taccagcgga accagcgctt ggagaaggcc ctgcagcagc tggcacgtgg ggacagcgcc 1620  
ggggagccct tggaggttga cctggaaggg gctgacatcc cctacgagga catcatagcc 1680  
actgagatct ga 1692

<210> 14

<211> 1722

<212> DNA

<213> Homo sapiens

<400> 14

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ctgcagcagc tggcacgtgg ggacagcgcc ggggagccct tggaggttga cctggaaggg 1680
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<210> 15

<211> 76

<212> PRT

<213> Homo sapiens

<400> 15

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Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
  1                   5                   10                   15

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```

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
    20                   25                   30

```

```

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
    35                   40                   45

```

```

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser
    50                   55                   60

```





195

200

205

Glu Ile

210

&lt;210&gt; 17

&lt;211&gt; 537

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys

1

5

10

15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys

20

25

30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln

35

40

45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp

50

55

60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro

65

70

75

80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val

85

90

95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln

100

105

110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys

115

120

125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser

130

135

140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln

145

150

155

160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg

165

170

175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln

180

185

190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly  
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met  
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly  
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile  
245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu  
260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu  
275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp  
290 295 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala  
305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu  
325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu  
340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg  
355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val  
370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu  
385 390 395 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys  
405 410 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg  
420 425 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
435 440 445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu  
450 455 460

Arg Glu Lys His Glu Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val  
465 470 475 480

Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln  
485 490 495

Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp  
500 505 510

Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro  
515 520 525

Tyr Glu Asp Ile Ile Ala Thr Glu Ile  
530 535

<210> 18

<211> 504

<212> PRT

<213> Homo sapiens

<400> 18

Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
 130 135 140  
 Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
 145 150 155 160  
 Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
 165 170 175  
 Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Tyr Gln  
 180 185 190  
 Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly  
 195 200 205  
 Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met  
 210 215 220  
 Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly  
 225 230 235 240  
 His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile  
 245 250 255  
 Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu  
 260 265 270  
 Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu  
 275 280 285  
 Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp  
 290 295 300  
 Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala  
 305 310 315 320  
 Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu  
 325 330 335  
 Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu  
 340 345 350  
 Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg  
 355 360 365  
 Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val  
 370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu  
385 390 395 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys  
405 410 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg  
420 425 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
435 440 445

Val Cys Glu Asn Glu Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg  
450 455 460

Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser  
465 470 475 480

Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr  
485 490 495

Glu Asp Ile Ile Ala Thr Glu Ile  
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<210> 19

<211> 563

<212> PRT

<213> Homo sapiens

<400> 19

Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
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His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val

95

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu

340	345	350
Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg		
355	360	365
Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val		
370	375	380
Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu		
385	390	395 400
Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys		
405	410	415
Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg		
420	425	430
Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu		
435	440	445
Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu		
450	455	460
Arg Glu Lys Val Asn Leu Leu Glu Arg Leu Arg Ala Glu Leu Arg Glu		
465	470	475 480
Glu Arg Gln Gly His Asp Gln Met Ser Ser Gly Phe Gln His Glu Arg		
485	490	495
Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln		
500	505	510
Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu		
515	520	525
Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu		
530	535	540
Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala		
545	550	555 560
Thr Glu Ile		

<210> 20  
 <211> 573  
 <212> PRT

<213> Homo sapiens

<400> 20

Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
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His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln  
180 185 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly  
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met  
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly  
225 230 235 240



His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile  
 245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu  
 260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu  
 275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp  
 290 295 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala  
 305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu  
 325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu  
 340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg  
 355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val  
 370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu  
 385 390 395 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys  
 405 410 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg  
 420 425 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
 435 440 445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu  
 450 455 460

Arg Glu Lys Val Asn Leu Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala  
 465 470 475 480

Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp  
 485 490 495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Val Trp Lys Glu Glu  
500 505 510

Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val  
515 520 525

Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu  
530 535 540

Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly  
545 550 555 560

Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr Glu Ile  
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<210> 21

<211> 591

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: F37 Probe

<400> 21

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tatgggggca tctcttcccc agagaggcac tcagtgagcc tcctgtgcct ggccccagtc 180  
tgggccatct cttaggtgag acagttgccc gaaactaagc caggcctggc tggaggagca 240  
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tgacagaggc tgcacccctg ggccagcggg gctgctcacc cacctcttgt gcaaggtggc 360  
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agcatctgga agatgtacat agttattttt ctctttgtgg tttcttggtt gggttggttt 480  
gcttttgaca gcttcatttt atttttgacg tcactttttg gccatgtaaa ctatttggtg 540  
caatttttat tttttattta tgaataaaga atgccatttc tcacgcctc t 591

<210> 22

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplificatin primer G12

<400> 22

gctgccacag cctttccaag acc

23

<210> 23  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G13

<400> 23  
taccggttga gcttcttgag gtg

23

<210> 24  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G14.2

<400> 24  
acagcttcca cagcaagcac tgc

23

<210> 25  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G15

<400> 25  
attggagaag ggcatgagct t

21

<210> 26  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable

region amplification primer G16

<400> 26  
tggactttga cccgtccaca cc 22

<210> 27  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer IntABR

<400> 27  
gtttccaacc cacttaccct tgc 23

<210> 28  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer IntABF

<400> 28  
gcaggggagg catgagtcac c 21

<210> 29  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G17

<400> 29  
ggcttcagct cctgctcctt gg 22

<210> 30  
<211> 23  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G20

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<211> 23

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<223> Description of Artificial Sequence: FEZ1 alterable  
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<210> 33

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer IntBCR

<400> 33

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<210> 34  
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<223> Description of Artificial Sequence: FEZ1 alterable  
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<210> 35  
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<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer Mut6

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<210> 36  
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<223> Description of Artificial Sequence: FEZ1 alterable  
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<223> Description of Artificial Sequence: FEZ1 alterable  
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<210> 41

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<223> Description of Artificial Sequence: FEZ1 alterable  
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<210> 44

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of partially-double stranded adapter-linker

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<210> 46  
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<223> Description of Artificial Sequence: Donor site  
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<210> 47  
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<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

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21

<210> 48  
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sequence of truncated FEZ1 truncation region

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<210> 49  
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<220>  
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sequence of truncated FEZ1 truncation region

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<223> Description of Artificial Sequence: Donor site  
sequence of truncated FEZ1 truncation region

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sequence of truncated FEZ1 truncation region

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<223> Description of Artificial Sequence: Donor site  
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<400> 52

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23

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

<400> 53

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<210> 54

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Donor site  
sequence of truncated FEZ1 truncation region

<400> 54

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23

<210> 55

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

<400> 55

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22

<210> 56

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<223> Description of Artificial Sequence: Primer for  
amplifying FEZ1 cDNA

<400> 58  
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<210> 59
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<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Primer for  
amplifying FEZ1 cDNA

36

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24

<210> 60

<211> 8073

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide  
sequence of vector pQBI-AdCMV5-IRES-GFP

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